

-1-

SEQUENCE LISTING

<110> Isis Innovation Limited

<120> Process for oxidising aromatic compounds

<130> N76277A PEJ

5 <170> PatentIn Ver. 2.1

<210> 1

<211> 1242

<212> DNA

<213> Pseudomonas putida

10 <220>

<221> CDS

<222> (1)..(1242)

<400> 1

acg act gaa acc ata caa agc aac gcc aat ctt gcc cct ctg cca ccc 48

15 Thr Thr Glu Thr Ile Gln Ser Asn Ala Asn Leu Ala Pro Leu Pro Pro

1 5 10 15

cat gtg cca gag cac ctg gta ttc gac ttc gac atg tac aat ccg tcg 96

His Val Pro Glu His Leu Val Phe Asp Phe Asp Met Tyr Asn Pro Ser

20 25 30

20 aat ctg tct gcc ggc gtg cag gag gcc tgg gca gtt ctg caa gaa tca 144

Asn Leu Ser Ala Gly Val Gln Glu Ala Trp Ala Val Leu Gln Glu Ser

35 40 45

aac gta ccg gat ctg gtg tgg act cgc tgc aac ggc gga cac tgg atc 192

Asn Val Pro Asp Leu Val Trp Thr Arg Cys Asn Gly Gly His Trp Ile

25 50 55 60

gcc act cgc ggc caa ctg atc cgt gag gcc tat gaa gat tac cgc cac 240

Ala Thr Arg Gly Gln Leu Ile Arg Glu Ala Tyr Glu Asp Tyr Arg His

65 70 75 80

ttt tcc agc gag tgc ccg ttc atc cct cgt gaa gcc ggc gaa gcc tac 288

30 Phe Ser Ser Glu Cys Pro Phe Ile Pro Arg Glu Ala Gly Glu Ala Tyr

85 90 95

-2-

gac ttc att ccc acc tcg atg gat ccg ccc gag cag cgc cag ttt cgt 336
 Asp Phe Ile Pro Thr Ser Met Asp Pro Pro Glu Gln Arg Gln Phe Arg
 100 105 110

5 gcg ctg gcc aac caa gtg gtt ggc atg ccg gtg gtg gat aag ctg gag 384
 Ala Leu Ala Asn Gln Val Val Gly Met Pro Val Val Asp Lys Leu Glu
 115 120 125

aac cgg atc cag gag ctg gcc tgc tcg ctg atc gag agc ctg cgc ccg 432
 Asn Arg Ile Gln Glu Leu Ala Cys Ser Leu Ile Glu Ser Leu Arg Pro
 130 135 140

10 caa gga cag tgc aac ttc acc gag gac tac gcc gaa ccc ttc ccg ata 480
 Gln Gly Gln Cys Asn Phe Thr Glu Asp Tyr Ala Glu Pro Phe Pro Ile
 145 150 155 160

cgc atc ttc atg ctg ctc gca ggt cta ccg gaa gaa gat atc ccg cac 528
 Arg Ile Phe Met Leu Leu Ala Gly Leu Pro Glu Glu Asp Ile Pro His
 15 165 170 175

ttg aaa tac cta acg gat cag atg acc cgt ccg gat ggc agc atg acc 576
 Leu Lys Tyr Leu Thr Asp Gln Met Thr Arg Pro Asp Gly Ser Met Thr
 180 185 190

20 ttc gca gag gcc aag gag gcg ctc tac gac tat ctg ata ccg atc atc 624
 Phe Ala Glu Ala Lys Glu Ala Leu Tyr Asp Tyr Leu Ile Pro Ile Ile
 195 200 205

gag caa cgc agg cag aag ccg gga acc gac gct atc agc atc gtt gcc 672
 Glu Gln Arg Arg Gln Lys Pro Gly Thr Asp Ala Ile Ser Ile Val Ala
 210 215 220

25 aac ggc cag gtc aat ggg cga ccg atc acc agt gac gaa gcc aag agg 720
 Asn Gly Gln Val Asn Gly Arg Pro Ile Thr Ser Asp Glu Ala Lys Arg
 225 230 235 240

WO 00/78973

PCT/GB00/02379

-3-

atg tgt ggc ctg tta ctg gtc ggc ggc ctg gat acg gtg gtc aat ttc 768
 Met Cys Gly Leu Leu Leu Val Gly Gly Leu Asp Thr Val Val Asn Phe
 245 250 255

5 ctc agc ttc agc atg gag ttc ctg gcc aaa agc ccg gag cat cgc cag 816
 Leu Ser Phe Ser Met Glu Phe Leu Ala Lys Ser Pro Glu His Arg Gln
 260 265 270

gag ctg atc gag cgt ccc gag cgt att cca gcc get tgc gag gaa cta 864
 Glu Leu Ile Glu Arg Pro Glu Arg Ile Pro Ala Ala Cys Glu Glu Leu
 275 280 285

10 ctc cgg cgc ttc tcg ctg gtt gcc gat ggc cgc atc ctc acc tcc gat 912
 Leu Arg Arg Phe Ser Leu Val Ala Asp Gly Arg Ile Leu Thr Ser Asp
 290 295 300

15 tac gag ttt cat ggc gtg caa ctg aag aaa ggt gac cag atc ctg cta 960
 Tyr Glu Phe His Gly Val Gln Leu Lys Lys Gly Asp Gln Ile Leu Leu
 305 310 315 320

ccg cag atg ctg tct ggc ctg gat gag cgc gaa aac gcc tgc ccg atg 1008
 Pro Gln Met Leu Ser Gly Leu Asp Glu Arg Glu Asn Ala Cys Pro Met
 325 330 335

20 cac gtc gac ttc agt cgc caa aag gtt tca cac acc acc ttt ggc cac 1056
 His Val Asp Phe Ser Arg Gln Lys Val Ser His Thr Thr Phe Gly His
 340 345 350

ggc agc cat ctg tgc ctt ggc cag cac ctg gcc cgc ccg gaa atc atc 1104
 Gly Ser His Leu Cys Leu Gly Gln His Leu Ala Arg Arg Glu Ile Ile
 355 360 365

25 gtc acc ctc aag gaa tgg ctg acc agg att cct gac ttc tcc att gcc 1152
 Val Thr Leu Lys Glu Trp Leu Thr Arg Ile Pro Asp Phe Ser Ile Ala
 370 375 380

WO 00/78973

PCT/GB00/02379

-4-

ccg ggt gcc cag att cag cac aag agc ggc atc gtc agc ggc gtg cag 1200
 Pro Gly Ala Gln Ile Gln His Lys Ser Gly Ile Val Ser Gly Val Gln
 385 390 395 400

5 gca ctc cct ctg gtc tgg gat ccg gcg act acc aaa gcg gta 1242
 Ala Leu Pro Leu Val Trp Asp Pro Ala Thr Thr Lys Ala Val
 405 410

<210> 2

<211> 3150

<212> DNA

10 <213> *Bacillus megaterium*

<220>

<221> CDS

<222> (1)..(3150)

<400> 2

15 atg aca att aaa gaa atg cct cag cca aaa acg ttt gga gag ctt aaa 48
 Met Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys
 1 5 10 15

aat tta ccg tta tta aac aca gat aaa ccg gtt caa gct ttg atg aaa 96
 Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys
 20 20 25 30

att gcg gat gaa tta gga gaa atc ttt aaa ttc gag gcg cct ggt cgt 144
 Ile Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg
 35 40 45

25 gta acg cgc tac tta tca agt cag cgt cta att aaa gaa gca tgc gat 192
 Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp
 50 55 60

gaa tca cgc ttt gat aaa aac tta agt caa gcg ctt aaa ttt gta cgt 240
 Glu Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg
 65 70 75 80

-5-

gat ttt gca gga gac ggg tta ttt aca agc tgg acg cat gaa aaa aat 288
 Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn
 85 90 95

tgg aaa aaa gcg cat aat atc tta ctt cca agc ttc agt cag cag gca 336
 5 Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala
 100 105 110

atg aaa ggc tat cat gcg atg atg gtc gat atc gcc gtg cag ctt gtt 384
 Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val
 115 120 125

10 caa aag tgg gag cgt cta aat gca gat gag cat att gaa gta ccg gaa 432
 Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu
 130 135 140

gac atg aca cgt tta acg ctt gat aca att ggt ctt tgc ggc ttt aac 480
 Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn
 15 145 150 155 160

tat cgc ttt aac agc ttt tac cga gat cag cct cat cca ttt att aca 528
 Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr
 165 170 175

20 agt atg gtc cgt gca ctg gat gaa gca atg aac aag ctg cag cga gca 576
 Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala
 180 185 190

aat cca gac gac cca gct tat gat gaa aac aag cgc cag ttt caa gaa 624
 Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu
 195 200 205

25 gat atc aag gtg atg aac gac cta gta gat aaa att att gca gat cgc 672
 Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg
 210 215 220

WO 00/78973

PCT/GB00/02379

-6-

aaa gca agc ggt gaa caa agc gat gat tta tta acg cat atg cta aac 720
 Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn
 225 230 235 240

gga aaa gat cca gaa acg ggt gag ccg ctt gat gac gag aac att cgc 768
 5 Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg
 245 250 255

tat caa att att aca ttc tta att gcg gga cac gaa aca aca agt ggt 816
 Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly
 260 265 270

10 ctt tta tca ttt gcg ctg tat ttc tta gtg aaa aat cca cat gta tta 864
 Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu
 275 280 285

caa aaa gca gca gaa gca gca cga gtt cta gta gat cct gct cca 912
 Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Ala Pro
 15 290 295 300

agc tac aaa caa gtc aaa cag ctt aaa tat gtc ggc atg gtc tta aac 960
 Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn
 305 310 315 320

20 gaa gcg ctg cgc tta tgg cca act gct cct gcg ttt tcc cta tat gca 1008
 Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala
 325 330 335

aaa gaa gat acg gtg ctt gga gga gaa tat cct tta gaa aaa ggc gac 1056
 Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp
 340 345 350

25 gaa cta atg gtt ctg att cct cag ctt cac cgt gat aaa aca att tgg 1104
 Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp
 355 360 365

-7-

gga gac gat gtg gaa gag ttc cgt cca gag cgt ttt gaa aat cca agt 1152
 Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser
 370 375 380

5 gcg att ccg cag cat gcg ttt aaa ccg ttt gga aac ggt cag cgt gcg 1200
 Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala
 385 390 395 400

tgt atc ggt cag cag ttc gct ctt cat gaa gca acg ctg gta ctt ggt 1248
 Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly
 405 410 415

10 atg atg cta aaa cac ttt gac ttt gaa gat cat aca aac tac gag ctg 1296
 Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu
 420 425 430

15 gat att aaa gaa act tta acg tta aaa cct gaa ggc ttt gtg gta aaa 1344
 Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys
 435 440 445

gca aaa tcg aaa aaa att ccg ctt ggc ggt att cct tca cct agc act 1392
 Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr
 450 455 460

20 gaa cag tct gcc aaa aaa gca cgc aaa aag gca gaa aac gct cat aat 1440
 Glu Gln Ser Ala Lys Lys Ala Arg Lys Lys Ala Glu Asn Ala His Asn
 465 470 475 480

acg ccg ctg ctt gtg cta tac ggt tca aat atg gga aca gct gaa gga 1488
 Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly
 485 490 495

25 acg gcg cgt gat tta gca gat att gca atg agc aaa gga ttt gca ccg 1536
 Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro
 500 505 510

-8-

cag gtc gca acg ctt gat tca cac gcc gga aat ctt ccg cgc gaa gga 1584
 Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly
 515 520 525

5 gct gta tta att gta acg gcg tct tat aac ggt cat ccg cct gat aac 1632
 Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn
 530 535 540

gca aag caa ttt gtc gac tgg tta gac caa gcg tct gct gat gaa gta 1680
 Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val
 545 550 555 560

10 aaa ggc gtt cgc tac tcc gta ttt gga tgc ggc gat aaa aac tgg gct 1728
 Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala
 565 570 575

15 act acg tat caa aaa gtg cct gct ttt atc gat gaa acg ctt gcc gct 1776
 Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala
 580 585 590

aaa ggg gca gaa aac atc gct gac cgc ggt gaa gca gat gca agc gac 1824
 Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp
 595 600 605

20 gac ttt gaa ggc aca tat gaa gaa tgg cgt gaa cat atg tgg agt gac 1872
 Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp
 610 615 620

gta gca gcc tac ttt aac ctc gac att gaa aac agt gaa gat aat aaa 1920
 Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys
 625 630 635 640

25 tct act ctt tca ctt caa ttt gtc gac agc gcc gcg gat atg ccg ctt 1968
 Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu
 645 650 655

WO 00/78973

PCT/GB00/02379

-9-

gcg aaa atg cac ggt gcg ttt tca acg aac gtc gta gca agc aaa gaa 2016
Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu
660 665 670

5 ctt caa cag cca ggc agt gca cga agc acg cga cat ctt gaa att gaa 2064
Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu
675 680 685

ctt cca aaa gaa gct tct tat caa gaa gga gat cat tta ggt gtt att 2112
 Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile
 690 695 700

10 cct cgc aac tat gaa gga ata gta aac cgt gta aca gca agg ttc ggc 2160
 Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly
 705 710 715 720

15 cta gat gca tca cag caa atc cgt ctg gaa gca gaa gaa gaa aaa tta 2208
 Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu
 725 730 735

20 tac gtg gag ctt caa gat cct gtt acg cgc acg cag ctt cgc gca atg 2304
 Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met
 755 760 765

gct gct aaa acg gtc tgc ccg ccg cat aaa gta gag ctt gaa gcc ttg 2352
Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu
770 775 780

25 ctt gaa aag caa gcc tac aaa gaa caa gtg ctg gca aaa cgt tta aca 2400
 Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr
 785 790 795 800

WO 00/78973

PCT/GB00/02379

-10-

atg ctt gaa ctg ctt gaa aaa tac ccg gcg tgt gaa atg aaa ttc agc 2448
 Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser
 805 810 815

5 gaa ttt atc gcc ctt ctg cca agc ata cgc ccg cgc tat tac tcg att 2496
 Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile
 820 825 830

tct tca tca cct cgt gtc gat gaa aaa caa gca agc atc acg gtc agc 2544
 Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser
 835 840 845

10 gtt gtc tca gga gaa gcg tgg agc gga tat gga gaa tat aaa gga att 2592
 Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile
 850 855 860

15 gcg tcg aac tat ctt gcc gag ctg caa gaa gga gat acg att acg tgc 2640
 Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys
 865 870 875 880

ttt att tcc aca ccg cag tca gaa ttt acg ctg cca aaa gac cct gaa 2688
 Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu
 885 890 895

20 acg ccg ctt atc atg gtc gga ccg gga aca ggc gtc gcg ccg ttt aga 2736
 Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg
 900 905 910

ggc ttt gtg cag gcg cgc aaa cag cta aaa gaa caa gga cag tca ctt 2784
 Gly Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu
 915 920 925

25 gga gaa gca cat tta tac ttc ggc tgc cgt tca cct cat gaa gac tat 2832
 Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr
 930 935 940

-11-

ctg tat caa gaa gag ctt gaa aac gcc caa agc gaa ggc atc att acg 2880
 Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr
 945 950 955 960

5 ctt cat acc gct ttt tct cgc atg cca aat cag ccg aaa aca tac gtt 2928
 Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val
 965 970 975

cag cac gta atg gaa caa gac ggc aag aaa ttg att gaa ctt ctt gat 2976
 Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp
 980 985 990

10 caa gga gcg cac ttc tat att tgc gga gac gga agc caa atg gca cct 3024
 Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro
 995 1000 1005

15 gcc gtt gaa gca acg ctt atg aaa agc tat gct gac gtt cac caa gtg 3072
 Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val
 1010 1015 1020

agt gaa gca gac gct cgc tta tgg ctg cag cag cta gaa gaa aaa ggc 3120
 Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly
 1025 1030 1035 1040

20 cga tac gca aaa gac gtg tgg gct ggg taa 3150
 Arg Tyr Ala Lys Asp Val Trp Ala Gly
 1045 1050